



1

SEQUENCE LISTING

RECEIVED

JAN 11 2002

TECH CENTER 1600 2900

(1) GENERAL INFORMATION:

- (i) APPLICANT: Golstein, Pierre
Rouvier, Eric
Fossiez, Francois
Lebecque, Serge J.E.
Djossou, Odile
Banchereau, Jacques
- (ii) TITLE OF INVENTION: Purified Mammalian CTLA-8 Antigens and Related Reagents
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Townsend and Townsend and Crew LLP
 - (B) STREET: Two Embarcadero Center, Eighth Floor
 - (C) CITY: San Francisco
 - (D) STATE: California
 - (E) COUNTRY: USA
 - (F) ZIP: 94111-3834
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 09/929,612
 - (B) FILING DATE: 13-AUG-2001
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/077,203
 - (B) FILING DATE: 14-JUN-1993
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/177,747
 - (B) FILING DATE: 05-JAN-1994
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/250,846
 - (B) FILING DATE: 27-MAY-1994
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/432,994
 - (B) FILING DATE: 02-MAY-1995
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/432,994
 - (B) FILING DATE: 22-JUN-1998
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Weber, Kenneth A.
 - (B) REGISTRATION NUMBER: 31,677
 - (C) REFERENCE/DOCKET NUMBER: 015631-003115US

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (415) 576-0200
 (B) TELEFAX: (415) 576-0300

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1080 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 12..464
 (D) OTHER INFORMATION: /product= "mouse/rat CTLA-8"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCATC C ATG TGC CTG ATG CTG TTG CTG CTA CTG AAC CTG GAG GCT 50
 Met Cys Leu Met Leu Leu Leu Leu Asn Leu Glu Ala
 1 5 10

ACA GTG AAG GCA GCG GTA CTC ATC CCT CAA AGT TCA GTG TGT CCA AAC 98
 Thr Val Lys Ala Ala Val Leu Ile Pro Gln Ser Ser Val Cys Pro Asn
 15 20 25

GCC GAG GCC AAT AAC TTT CTC CAG AAC GTG AAG GTC AAC CTG AAA GTC 146
 Ala Glu Ala Asn Asn Phe Leu Gln Asn Val Lys Val Asn Leu Lys Val
 30 35 40 45

ATC AAC TCC CTT AGC TCA AAA GCG AGC TCC AGA AGG CCC TCA GAC TAC 194
 Ile Asn Ser Leu Ser Ser Lys Ala Ser Ser Arg Arg Pro Ser Asp Tyr
 50 55 60

CTC AAC CGT TCC ACT TCA CCC TGG ACT CTG AGC CGT AAT GAG GAC CCT 242
 Leu Asn Arg Ser Thr Ser Pro Trp Thr Leu Ser Arg Asn Glu Asp Pro
 65 70 75

GAT AGA TAT CCT TCT GTG ATC TGG GAG GCA CAG TGC CGC CAC CAG CGC 290
 Asp Arg Tyr Pro Ser Val Ile Trp Glu Ala Gln Cys Arg His Gln Arg
 80 85 90

TGT GTC AAC GCT GAG GGG AAG TTG GAC CAC CAC ATG AAT TCT GTT CTC 338
 Cys Val Asn Ala Glu Gly Lys Leu Asp His His Met Asn Ser Val Leu
 95 100 105

ATC CAG CAA GAG ATC CTG GTC CTG AAG AGG GAG CCT GAG AAG TGC CCC 386
 Ile Gln Gln Glu Ile Leu Val Leu Lys Arg Glu Pro Glu Lys Cys Pro
 110 115 120 125

TTC ACT TTC CGG GTG GAG AAG ATG CTG GTG GGC GTG GGC TGC ACC TGC 434
 Phe Thr Phe Arg Val Glu Lys Met Leu Val Gly Val Gly Cys Thr Cys
 130 135 140

GTT TCC TCT ATT GTC CGC CAT GCG TCC TAAACAGAGA CCTGAGGCTA 481
 Val Ser Ser Ile Val Arg His Ala Ser
 145 150

GGCCCTAAGA AACCCCTGCG TTTCTCTGCA AATTCCTTG TCTTTTAAA ACAGTTCACA 541
 GTTGAATCTC AGCAAGTGAT ATGGATTAA AGGCGGCGTT AGAATTGTCT GCTTCCACC 601
 CTGAAAAGAA GCGCAGAGG GGATATAAAT TGCTCTTGT TTTCTGTGG GCTTTAAATT 661
 ATTTATGTAT TTAATCTATC CCGAGATAAC TTGAGGCAT AATTTATTTT AATGAATTAT 721
 CTACATTATT ATTATGTTTC TTAATGCAGA AGACAAAATT CAAGACTAAG AAATTTTATT 781
 ATTTAAAAGG TAAACCTAT ATTTATATGA GGTATTTATG GGTCTATTTA TTTTCTTCA 841
 GTGCTAAGAT CATGATTATC AGATCTACTT AAGGAACTCC TAAATAATAT TAAATATTAA 901
 TTGAAATTTT AGTTTTACTA TTTGCTTATT TAAGCTTCCC TCCTCTGAAT GGTGTGAAAT 961
 CAAACCTCGT TTTATGTTTT TAAATATTTG AGGCTTCGAA AAATTGGGCA ATTTAGCTTC 1021
 CTACTGTGTG TTTAAAAACC TTGTAACAAT ATCACTATAA TAAATTTTGT GAAGAAAAT 1080

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Cys Leu Met Leu Leu Leu Leu Asn Leu Glu Ala Thr Val Lys
 1 5 10 15
 Ala Ala Val Leu Ile Pro Gln Ser Ser Val Cys Pro Asn Ala Glu Ala
 20 25 30
 Asn Asn Phe Leu Gln Asn Val Lys Val Asn Leu Lys Val Ile Asn Ser
 35 40 45
 Leu Ser Ser Lys Ala Ser Ser Arg Arg Pro Ser Asp Tyr Leu Asn Arg
 50 55 60
 Ser Thr Ser Pro Trp Thr Leu Ser Arg Asn Glu Asp Pro Asp Arg Tyr
 65 70 75 80
 Pro Ser Val Ile Trp Glu Ala Gln Cys Arg His Gln Arg Cys Val Asn
 85 90 95
 Ala Glu Gly Lys Leu Asp His His Met Asn Ser Val Leu Ile Gln Gln
 100 105 110
 Glu Ile Leu Val Leu Lys Arg Glu Pro Glu Lys Cys Pro Phe Thr Phe
 115 120 125

Arg Val Glu Lys Met Leu Val Gly Val Gly Cys Thr Cys Val Ser Ser
 130 135 140

Ile Val Arg His Ala Ser
 145 150

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2520 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1574..2029
- (D) OTHER INFORMATION: /product= "Saimiriine herpesvirus 2
 immediate-early protein"
 /note= "open reading frame 2 (ORF2)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGCTTCATGC AAATACATCT TATCTTACCA GATTCTCGCC TCATTTGCAA ACATGCCTCA 60
 TCTTTTGAGA AGAAACGCAA TTCGAACCTC TTCTAATGCT CCTGAAGAGC AGCCTGTGCT 120
 GCAGCCTGAG CTTGATGCTA TTGAAGAGCT AGAATAAGAG CTATTTTTTG ACGATGGGTG 180
 CTGCCTTTCT GTTCAAGAAA TCTGCTTAAT TGTCTTGGA TTCTTATTGT TTCTGCTAGC 240
 TGTAATTGTT TTTTATAACT ATACAGACAC AGATCAATTT GTGAAGCTGA CACATCTTAT 300
 GAGCCACAAA AATTCTATCA AAGGACCTTT TGATCTTTAA GGTATGTACT CATAATTTTA 360
 TTTTTTTATT TCTAAACAA TCTTAGTATA TATAATTAAT ACAAATTTTA GAAAATACTA 420
 TAATAAATAT TGAAAGCTGT ATTTACATTG TAACTATAT ATAGGCAATG TAAAGTCATT 480
 CTAACCTTAG GTTTGCTTTA CCTGTTACAG AAACCTCACC TGTGTGTCAA GAGCTGCAAA 540
 CATGGCTTTA GACTTAAGAA ATCTTAAACA CCTGACTGCT AACTTCAGTT TTAGAATAAT 600
 GATATGGATT ATGCTATGTT TGGCTCTACC TACTGATAGT AAACCTATTT CAACAACTGA 660
 AGCTCCAATA CTAAACATAA CACAATCTCC AAGTTTGAAC ATCTCATCAC CTTCTACTTT 720
 AGAACCTTCA GAGCCTCTTA AAAACTGTAC AACATTCTTA GACTTACTTT GGCAGCGGCT 780
 GGGCGAGAAC GCTTCTATAA AGGACTTGAT GTTAACATTA CAACGAGAAG AAGTCCACGG 840
 AAGAATGACT ACACTTCCTT CACCTAGACC AAGCAGTAAA GTTGAAGAAC AACAGTTACA 900
 AAGACCTAGA AACTTACTGC CTAAGTCTGT CGGGCCACCT CATGTCAAAT ATAGACTATA 960
 TAATCGCTTA TGGGAAGCTC CTAAAGGAGC TGATGTTAAT GGTAACCTA TACAATTTGA 1020

TGACCTCCT CTTCCTTATA CAGGGGCATA TAATGATGAT GGTGTTTTAA TGGTTAATAT 1080
 TAATGGAAAA CATGTGAGGT TTGATAGCTT GTCTTATTGG GAAAGAATTA AAAGATCTGG 1140
 TACCCCATGG TGTATAAAGA CACCAAGTGA AAAAGCAGCA ATATTGAAGC AGCTTTTAAA 1200
 AGCTGAAAAA AAATGTAGGA CTACTTCTAA ACGTATCACT GAGTTAGAAG AGCAGATTAA 1260
 AGAACTAGAA AAAACTAGTA CATCTCCATA GATTACTGTT AGAATGTGTT TATCATACTA 1320
 AAATAAATGC TTTATGTATT GCAATATTAC TTGTTTGCTA TGACTTTGGT ATATGAAATG 1380
 CAAATCTTAA ATAAAAAGTT TTTGTCTAGT ATTGGCGTCA CTGTATTTTA CTAGCAAAAA 1440
 TATATAAATT GTTATGTAGC AAGAAGTTG TATCAATATA AAAACTCTAA AGTATATAAA 1500
 CAAACATTCA ATTAGTGTAA ATCATAGCAA GCATATCTTT TCATACGTGT CTAGTTAATT 1560
 TAAAGAATTA ATT ATG ACA TTT AGA ATG ACT TCA CTT GTG TTA CTT CTG 1609
 Met Thr Phe Arg Met Thr Ser Leu Val Leu Leu Leu
 1 5 10
 CTG CTG AGC ATA GAT TGT ATA GTA AAG TCA GAA ATA ACA AGC GCA CAA 1657
 Leu Leu Ser Ile Asp Cys Ile Val Lys Ser Glu Ile Thr Ser Ala Gln
 15 20 25
 ACC CCA AGA TGC TTA GCT GCT AAC AAT AGC TTT CCA CGG TCT GTG ATG 1705
 Thr Pro Arg Cys Leu Ala Ala Asn Asn Ser Phe Pro Arg Ser Val Met
 30 35 40
 GTT ACT TTG AGC ATC CGT AAC TGG AAT ACT AGT TCT AAA AGG GCT TCA 1753
 Val Thr Leu Ser Ile Arg Asn Trp Asn Thr Ser Ser Lys Arg Ala Ser
 45 50 55 60
 GAC TAC TAC AAT AGA TCT ACG TCT CCT TGG ACT CTC CAT CGC AAT GAA 1801
 Asp Tyr Tyr Asn Arg Ser Thr Ser Pro Trp Thr Leu His Arg Asn Glu
 65 70 75
 GAT CAA GAT AGA TAT CCC TCT GTG ATT TGG GAA GCA AAG TGT CGC TAC 1849
 Asp Gln Asp Arg Tyr Pro Ser Val Ile Trp Glu Ala Lys Cys Arg Tyr
 80 85 90
 TTA GGA TGT GTT AAT GCT GAT GGG AAT GTA GAC TAC CAC ATG AAC TCA 1897
 Leu Gly Cys Val Asn Ala Asp Gly Asn Val Asp Tyr His Met Asn Ser
 95 100 105
 GTC CCT ATC CAA CAA GAG ATT CTA GTG BTG CGC AAA GGG CAT CAA CCC 1945
 Val Pro Ile Gln Gln Glu Ile Leu Val Val Arg Lys Gly His Gln Pro
 110 115 120
 TGC CCT AAT TCA TTT AGG CTA GAG AAG ATG CTA GTG ACT GTA GGC TGC 1993
 Cys Pro Asn Ser Phe Arg Leu Glu Lys Met Leu Val Thr Val Gly Cys
 125 130 135 140
 ACA TGC GTT ACT CCC ATT GTT CAC AAT GTA GAC TAAAAGCTAT CTAAATTTTG 2046
 Thr Cys Val Thr Pro Ile Val His Asn Val Asp
 145 150
 AAAATTAACA TTCACTAAA AAACAAAAAC TTGATTTTTT TCTTTTAAAT AAAAAAGTT 2106
 TAATATAAGT TCTGGCTTGT TTGGTTTTTG ACTAATCAAT GTAGATCACA CTTGTGATCT 2166

TAGCTCTGG GAAGCAATGT AAGAAAATAT ATTTAACTTA AGAGTTTGTAG ACTTGTTGA 2226
 GTTTTATGAG TAAAAACAA AGAATAAGCA CAGCTTCTTG TATCTTCTTT TAAAACTTT 2286
 AAGTTATTTA TGTATTTAAT ATAATCTAAT GTTTCTTAAA CATGTTGAGT TTGAGGTCCA 2346
 CTAATACAAC ATTATAATTT TTTCTGTTAT AACACTTTTG CAAGAAGAAC TCATTTTATA 2406
 GAAAATGAGC AGTATTCAAA AAAAATGTTT GATATGCTGT AATATTGGAG AGGAAAGAACT 2466
 TTTACAABCA TGTGATTGTC CTAGCAGAGT CCATCATACA TGCITACAAA GTCA 2520

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Thr Phe Arg Met Thr Ser Leu Val Leu Leu Leu Leu Ser Ile
 1 5 10 15
 Asp Cys Ile Val Lys Ser Glu Ile Thr Ser Ala Gln Thr Pro Arg Cys
 20 25 30
 Leu Ala Ala Asn Asn Ser Phe Pro Arg Ser Val Met Val Thr Leu Ser
 35 40 45
 Ile Arg Asn Trp Asn Thr Ser Ser Lys Arg Ala Ser Asp Tyr Tyr Asn
 50 55 60
 Arg Ser Thr Ser Pro Trp Thr Leu His Arg Asn Glu Asp Gln Asp Arg
 65 70 75 80
 Tyr Pro Ser Val Ile Trp Glu Ala Lys Cys Arg Tyr Leu Gly Cys Val
 85 90 95
 Asn Ala Asp Gly Asn Val Asp Tyr His Met Asn Ser Val Pro Ile Gln
 100 105 110
 Gln Glu Ile Leu Val Val Arg Lys Gly His Gln Pro Cys Pro Asn Ser
 115 120 125
 Phe Arg Leu Glu Lys Met Leu Val Thr Val Gly Cys Thr Cys Val Thr
 130 135 140
 Pro Ile Val His Asn Val Asp
 145 150

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..237
- (D) OTHER INFORMATION: /product= "human CTLA-8 fragment"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

MGC AAT GAG GAC CCT GAG AGA TAT CCC TCT GTG ATC TGG GAG GCA AAG 48
Xaa Asn Glu Asp Pro Glu Arg Tyr Pro Ser Val Ile Trp Glu Ala Lys
1 5 10 15
TGC CGC CAC TTG GGC TGC ATC AAC GCT GAT GGG AAC GTG GAC TAC CAC 96
Cys Arg His Leu Gly Cys Ile Asn Ala Asp Gly Asn Val Asp Tyr His
20 25 30
ATG AAC TCT GTC CCC ATC CAG CAA GAG ATC CTG GTC CTG CGC AGG GAG 144
Met Asn Ser Val Pro Ile Gln Gln Glu Ile Leu Val Leu Arg Arg Glu
35 40 45
CCT CCA CAC TGC CCC AAC TCC TTC CGG CTG GAG AAG ATA CTG GTG TCC 192
Pro Pro His Cys Pro Asn Ser Phe Arg Leu Glu Lys Ile Leu Val Ser
50 55 60
GTG GGC TGC ACC TGT GTC ACC CCG ATT GTC CAC CAT GTG GCC 234
Val Gly Cys Thr Cys Val Thr Pro Ile Val His His Val Ala
65 70 75
TAA 237

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Ser or Arg"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Xaa Asn Glu Asp Pro Glu Arg Tyr Pro Ser Val Ile Trp Glu Ala Lys
1 5 10 15

Cys Arg His Leu Glv Cys Ile Asn Ala Asp Gly Asn Val Asp Tyr His
20 25 30

Met Asn Ser Val Pro Ile Gln Gln Glu Ile Leu Val Leu Arg Arg Glu
35 40 45

Pro Pro His Cys Pro Asn Ser Phe Arg Leu Glu Lys Ile Leu Val Ser
50 55 60

Val Gly Cys Thr Cys Val Thr Pro Ile Val His His Val Ala
65 70 75

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 510 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1.510
(D) OTHER INFORMATION: /note= "full length human CTLA 8 clone"

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 43..510
(D) OTHER INFORMATION: /product= "human CTLA-8"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

[illegible]

TAT CCC TCT GTG ATC TGG GAG GCA AAG TGC CGC CAC TTG GGC TGC ATC 342
 Tyr Pro Ser Val Ile Trp Glu Ala Lys Cys Arg His Leu Gly Cys Ile
 85 90 95 100
 AAC GCT GAT GGG AAC GTG GAC TAC CAC ATG AAC TCT GTC CCC ATC CAG 390
 Asn Ala Asp Gly Asn Val Asp Tyr His Met Asn Ser Val Pro Ile Gln
 105 110 115
 CAA GAG ATC CTG GTC CTG CGC AGG GAG CCT CCA CAC TGC CCC AAC TCC 438
 Gln Glu Ile Leu Val Leu Arg Arg Glu Pro Pro His Cys Pro Asn Ser
 120 125 130
 TTC CGG CTG GAG AAG ATA CTG GTG TCC GTG GGC TGC ACC TGT GTC ACC 486
 Phe Arg Leu Glu Lys Ile Leu Val Ser Val Gly Cys Thr Cys Val Thr
 135 140 145
 CCG ATT GTC CAC CAT GTG GCC TAA 510
 Pro Ile Val His His Val Ala
 150 155

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
 (B) TYPE: amino acid
 (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Thr Pro Gly Lys Thr Ser Leu Val Ser Leu Leu Leu Leu Leu Ser
 1 5 10 15
 Leu Glu Ala Ile Val Lys Ala Gly Ile Thr Ile Pro Arg Asn Pro Gly
 20 25 30
 Cys Pro Asn Ser Glu Asp Lys Asn Phe Pro Arg Thr Val Met Val Asn
 35 40 45
 Leu Asn Ile His Asn Arg Asn Thr Asn Thr Asn Pro Lys Arg Ser Ser
 50 55 60
 Asp Tyr Tyr Asn Arg Ser Thr Ser Pro Trp Asn Leu His Arg Asn Glu
 65 70 75 80
 Asp Pro Glu Arg Tyr Pro Ser Val Ile Trp Glu Ala Lys Cys Arg His
 85 90 95
 Leu Gly Cys Ile Asn Ala Asp Gly Asn Val Asp Tyr His Met Asn Ser
 100 105 110
 Val Pro Ile Gln Gln Glu Ile Leu Val Leu Arg Arg Glu Pro Pro His
 115 120 125
 Cys Pro Asn Ser Phe Arg Leu Glu Lys Ile Leu Val Ser Val Gly Cys
 130 135 140
 Thr Cys Val Thr Pro Ile Val His His Val Ala
 145 150 155

GAGGCTCAAG	TGCACCCAGC	ACCAGCTGAT	CAGGACGGCG	AAAC	ATG AGT CCA GGG		56
					Met Ser Pro Gly		
					1		
AGA GCT TCA TCT GTG TCT CTG ATG CTG TTG CTG CTG CTG AGC CTG GCG							104
Arg Ala Ser Ser Val Ser Leu Met Leu Leu Leu Leu Leu Ser Leu Ala							
5				10		15	20
GCT ACA GTG AAG GCA GCA GCG ATC ATC CCT CAA AGC TCA GCG TGT CCA							152
Ala Thr Val Lys Ala Ala Ala Ile Ile Pro Gln Ser Ser Ala Cys Pro							
		25				30	35
AAC ACT GAG GCC AAG GAC TTC CTC CAG AAT GTG AAG GTC AAC CTC AAA							200
Asn Thr Glu Ala Lys Asp Phe Leu Gln Asn Val Lys Val Asn Leu Lys							
		40				45	50
GTC TTT AAC TCC CTT GGC GCA AAA GTG AGC TCC AGA AGG CCC TCA GAC							248
Val Phe Asn Ser Leu Gly Ala Lys Val Ser Ser Arg Arg Pro Ser Asp							
		55				60	65
TAC CTC AAC CGT TCC ACG TCA CCC TGG ACT CTC CAC CGC AAT GAA GAC							296
Tyr Leu Asn Arg Ser Thr Ser Pro Trp Thr Leu His Arg Asn Glu Asp							
		70				75	80
CCT GAT AGA TAT CCC TCT GTG ATC TGG GAA GCT CAG TGC CGC CAC CAG							344
Pro Asp Arg Tyr Pro Ser Val Ile Trp Glu Ala Gln Cys Arg His Gln							
85				90			100
CGC TGT GTC AAT GCG GAG GGA AAG CTG GAC CAC CAC ATG AAT TCT GTT							392
Arg Cys Val Asn Ala Glu Gly Lys Leu Asp His His Met Asn Ser Val							
				105			110
							115
CTC ATC CAG CAA GAG ATC CTG GTC CTG AAG AGG GAG CCT GAG AGC TGC							440
Leu Ile Gln Gln Glu Ile Leu Val Leu Lys Arg Glu Pro Glu Ser Cys							
				120			125
							130

CCC TTC ACT TTC AGG GTC GAG AAG ATG CTG GTG GGT GTG GGC TGC ACC 488
 Pro Phe Thr Phe Arg Val Glu Lys Met Leu Val Gly Val Gly Cys Thr
 135 140 145

TGC GTG GCC TCG ATT GTC CGC CAG GCA GCC TAAACAGAGA CCCGCGGCTG 538
 Cys Val Ala Ser Ile Val Arg Gln Ala Ala
 150 155

ACCCCTAAGA AACCCCCACG TTTCTCAGCA AACTTACTTG CATTITTAAA ACAGTTCGTG 598

CTATTGATTT TCAGCAAGGA ATGTGGATTC AGAGGCAGAT TCAGAATTGT CTGCCCTCCA 658

CAATGAAAAG AAGGTGTAAA GGGGTCCCAA ACTGCTTCGT GTTGTTTTTT CTGTGGACTT 718

TAAATTATTT GTGTATTTAC AATATCCCAA GATAACTTTG AAGGCGTAAC TTATTTAATG 778

AAGTATCTAC ATTATTATTA TGTTTCCTTC TGAAGAAGAC AAAATTCAAG ACTCAGAAAT 838

TTTATTATTT AAAAGGTAAG CCTATATTTA TATGAGCTAT TTAIGAATCT ATTTATTTTT 898

CTTCAGTATT TGAAGTATTA AGAACATGAT TTTCAGATCT ACCTAGGGAA GTCCTAAGTA 958

AGATTAAATA TTAATGGAAA TTTCAGCTTT ACTATTTGGT TGATTTAAGG TTCTCTCCTC 1018

TGAATGGGGT GAAAACCAAA CTTAGTTTTA TGTTTAATAA CTTTTTAAAT TATTGAAGAT 1078

TCAAAAAATT GGATAATTTA GCTCCCTACT CTGTTTTAAA AAAAAAAAAA AAAAAA 1134

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Ser Pro Gly Arg Ala Ser Ser Val Ser Leu Met Leu Leu Leu Leu
 1 5 10 15
 Leu Ser Leu Ala Ala Thr Val Lys Ala Ala Ala Ile Ile Pro Gln Ser
 20 25 30
 Ser Ala Cys Pro Asn Thr Glu Ala Lys Asp Phe Leu Gln Asn Val Lys
 35 40 45
 Val Asn Leu Lys Val Phe Asn Ser Leu Gly Ala Lys Val Ser Ser Arg
 50 55 60
 Arg Pro Ser Asp Tyr Leu Asn Arg Ser Thr Ser Pro Trp Thr Leu His
 65 70 75 80
 Arg Asn Glu Asp Pro Asp Arg Tyr Pro Ser Val Ile Trp Glu Ala Gln
 85 90 95
 Cys Arg His Gln Arg Cys Val Asn Ala Glu Gly Lys Leu Asp His His
 100 105 110

Met Asn Ser Val Leu Ile Gln Gln Glu Ile Leu Val Leu Lys Arg Glu
115 120 125

Pro Glu Ser Cys Pro Phe Thr Phe Arg Val Glu Lys Met Leu Val Gly
130 135 140

Val Gly Cys Thr Cys Val Ala Ser Ile Val Arg Gln Ala Ala
145 150 155